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NEWS 5 AUG 30 CA(SM)/CAPLUS(SM) Austrian patent law changes
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NEWS 7 SEP 21 CA/CAPLUS fields enhanced with simultaneous left and right truncation
NEWS 8 SEP 25 CA(SM)/CAPLUS(SM) display of CA Lexicon enhanced
NEWS 9 SEP 25 CAS REGISTRY(SM) no longer includes Concord 3D coordinates
NEWS 10 SEP 25 CAS REGISTRY(SM) updated with amino acid codes for pyrrolysine
NEWS 11 SEP 28 CEABA-VTB classification code fields reloaded with new classification scheme
NEWS 12 OCT 19 LOGOFF HOLD duration extended to 120 minutes
NEWS 13 OCT 19 E-mail format enhanced
NEWS 14 OCT 23 Option to turn off MARPAT highlighting enhancements available
NEWS 15 OCT 23 CAS Registry Number crossover limit increased to 300,000 in multiple databases
NEWS 16 OCT 23 The Derwent World Patents Index suite of databases on STN has been enhanced and reloaded
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NEWS 18 NOV 03 JAPIO enhanced with IPC 8 features and functionality

NEWS EXPRESS JUNE 30 CURRENT WINDOWS VERSION IS V8.01b, CURRENT MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP), AND CURRENT DISCOVER FILE IS DATED 26 JUNE 2006.

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NEWS IPC8 For general information regarding STN implementation of IPC 8
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FILE LAST UPDATED: 6 Nov 2006 (20061106/ED)

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=> s (circular?(10a)(array? or microarray?))/bi,ab 104885
CIRCULAR?/BI 79574 CIRCULAR?/AB
156047 ARRAY?/BI 145277 ARRAY?/AB
44665 MICROARRAY?/BI 25404 MICROARRAY?/AB
L1 779 (CIRCULAR?(10A)(ARRAY? OR
MICROARRAY?))/BI,AB

=> s phagemid?/bi,ab 1165 PHAGEMID?/BI
833 PHAGEMID?/AB
L2 1165 PHAGEMID?/BI,AB

=> s l1 and l2
L3 1 L1 AND L2

=> d l3 bib ab

L3 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:120940 CAPLUS <<LOGINID::20061108>>
DN 140:176210
TI Use of vectors forming single-stranded sense
circular DNAs as probes for ***array*** hybridization
IN Park, Jong-Gu; Lee, Yun-Han
PA Welgene Pharmaceuticals, Inc., S. Korea
SO PCT Int. Appl., 38 pp. CODEN: PIXXD2
DT Patent
LA English

FAN.CNT	1 PATENT NO.	KIND	DATE	APPLICATION
NO.	DATE			

PI	WO 2004013277	A2	20040212	WO 2003-IB4955
	20030725	WO 2004013277	A3	20040603 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,

CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG KR 2004011602 A 20040211 KR 2002-44411 20020727 CA 2493791 AA 20040212 CA 2003-2493791 20030725 AU 2003274587 A1 20040223 AU 2003-274587 20030725 US 2004038280 A1 20040226 US 2003-627882 20030725 EP 1543167 A2 20050622 EP 2003-758562 20030725 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK CN 1678758 A 20051005 CN 2003-820929 20030725 JP 2006503558 T2 20060202 JP 2004-525717 20030725 PRAI KR 2002-44411 A 20020727 WO 2003-IB4955 W 20030725 AB A method of generating long probes for use in microarray hybridization by propagating the cloned sequences in vectors capable of generating a circular single-stranded sense DNA is described. These probes, which may be several thousand bases, are hybridized against a cDNA population to detect differences in expression profiles between cell populations. Use of ***phagemids*** to create probes from a nonredundant library on silanized slides is demonstrated. By hybridization of the sense array with Cy3 or Cy5-labeled cDNA preps. at 60 .degree.C , 29 up-regulated and 6 down-regulated genes in cancerous liver tissue were detected.

=> s l1 not 2006/py 1112423 2006/PY
L4 701 L1 NOT 2006/PY

=> s l4 not 2005/py 1362126 2005/PY
L5 640 L4 NOT 2005/PY

=> s l5 not 2004/py 1321994 2004/PY
L6 569 L5 NOT 2004/PY

=> s l6 and (dna#1 or cdna# or (nucleic(w)acid#))/bi,ab
' TRUNCATION SYMBOL NOT VALID WITHIN 'DNA#1'
The truncation symbol # may be used only at the end of a search term.
To specify a variable character within a word use '!', e.g., 'wom!n'
to search for both 'woman' and 'women'. Enter "HELP TRUNCATION" at an arrow prompt (=>) for more information.

=> s l6 and (dna# or cdna# or (nucleic(w)acid#))/bi,ab
804859 DNA#/BI 622096 DNA#/AB
204460 CDNA#/BI 159210 CDNA#/AB
189751 NUCLEIC/BI 79175 NUCLEIC/AB
4737880 ACID#/BI 3186046 ACID#/AB
188731 NUCLEIC(W)ACID#
L7 24 L6 AND (DNA# OR CDNA# OR
(NUCLEIC(W)ACID#))/BI,AB

=> d his
(FILE 'HOME' ENTERED AT 09:39:09 ON 08 NOV 2006)
FILE 'CAPLUS' ENTERED AT 09:39:26 ON 08 NOV 2006

L1 779 S (CIRCULAR?(10A)(ARRAY? OR
MICROARRAY?))/BI,AB
L2 1165 S PHAGEMID?/BI,AB
L3 1 S L1 AND L2
L4 701 S L1 NOT 2006/PY
L5 640 S L4 NOT 2005/PY
L6 569 S L5 NOT 2004/PY
L7 24 S L6 AND (DNA# OR CDNA# OR
(NUCLEIC(W)ACID#))/BI,AB

=> d l7 1-24 bib ab

L7 ANSWER 1 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:272957 CAPLUS <<LOGINID::20061108>>
DN 139:306160
TI Anti-tumor effect of in vivo IL-2 and GM-CSF electrogene
therapy in murine hepatoma model.
AU Chi, Chau-Hwa; Wang, Yu-Shan; Lai, Yen-Shuae; Chi, Kwan-
Hwa
CS Department of Veterinary Medicine, National Taiwan
University, Taiwan
SO Anticancer Research (2003), 23(1A), 315-321 CODEN:
ANTRD4; ISSN: 0250-7005
PB International Institute of Anticancer Research
DT Journal
LA English
AB The authors evaluated the effect of in vivo electrogene
therapy (EGT), a newly-developed gene transfer method using
electroporation on the induction of anti-cancer immunity. The in
vivo EGT was carried out by direct injection of plasmid
DNAs encoding mouse interleukin-2 (IL-2) and
granulocyte-macrophage colony-stimulating factor (GM-CSF) in a
s.c. murine hepatoma model of 1MEA.7R.1 cells. Six elec. pulses
were generated in situ from a square-wave electroporator fitted
with a ***circular***, six-needle electrode ***array***.
1MEA.7R.1 cells in vitro were modified to secrete IL-2
(1MEA.7R.1/IL-2 cells). The 1MEA.7R.1/IL-2 cells had a similar
cell doubling-time as their parent cells but showed a much slower
growth rate in Balb/C mice. One, or 3 rounds of single gene EGT
with IL-2 gene showed a dose-responsive effect of growth
retardation. Co-administration of 3 rounds of IL-2/GM-CSF
double gene EGT had a stronger growth inhibition effect than 3
rounds of IL-2 single gene EGT. Three rounds of IL-2/GM-CSF
EGT rendered the tumor to a growth rate of stably transfected
1MEA.7R.1/IL-2 cells. Seven rounds of IL-2/GM-CSF EGT
markedly inhibited the tumor growth. Reverse transcriptase-
polymerase chain reaction confirmed the expression of IL-2, GM-
CSF and interferon-gamma. within treated tumors. Systemic
inhibitory effects can be demonstrated from tumor-re-challenged
expts. on mice which received 3 rounds of double-gene EGT.
The T cell proliferation assay revealed an increased T cell
proliferation in double-gene EGT-treated mice. This expt.
showed that partial systemic immunity can be provoked by IL-
2/GM-CSF double-gene EGT. These findings suggest that the
immuno-gene therapy protocol has the potential for future clin.
applications.
RE.CNT 26 THERE ARE 26 CITED REFERENCES AVAILABLE
FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE
FORMAT

L7 ANSWER 2 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:735332 CAPLUS <<LOGINID::20061108>>
DN 138:34036
TI Acetylation of histone H4 by Esa1 is required for
DNA double-strand break repair

AU Bird, Alexander W.; Yu, David Y.; Pray-Grant, Marilyn G.;
Qiu, Qifeng; Harmon, Kirsty E.; Megee, Paul C.; Grant, Patrick A.;
Smith, M. Mitchell; Christman, Michael F.
CS Department of Microbiology, University of Virginia,
Charlottesville, VA, 22908, USA

SO Nature (London, United Kingdom) (2002), 419(6905), 411-
415 CODEN: NATUAS; ISSN: 0028-0836

PB Nature Publishing Group

DT Journal

LA English

AB Although the acetylation of histones has a well-documented
regulatory role in transcription, its role in other chromosomal
functions remains largely unexplored. Here we show that distinct
patterns of histone H4 acetylation are essential in two sep.
pathways of double-strand break repair. A budding yeast strain
with mutations in wild-type H4 acetylation sites shows defects in
nonhomologous end joining repair and in a newly described
pathway of replication-coupled repair. Both pathways require the
Esa1 histone acetyl transferase (HAT), which is responsible for
acetylating all H4 tail lysines, including ectopic lysines that
restore repair capacity to a mutant H4 tail. Arp4, a protein that
binds histone H4 tails and is part of the Esa1-contg. NuA4 HAT
complex, is recruited specifically to ***DNA*** double-strand
breaks that are generated in vivo. The purified Esa1-Arp4 HAT
complex acetylates linear nucleosomal ***arrays*** with far
greater efficiency than ***circular*** ***arrays*** in
vitro, indicating that it preferentially acetylates nucleosomes near
a break site. Together, our data show that histone tail
acetylation is required directly for ***DNA*** repair and
suggest that a related human HAT complex may function
similarly.

RE.CNT 47 THERE ARE 47 CITED REFERENCES AVAILABLE
FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE
FORMAT

L7 ANSWER 3 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN

AN 2002:715961 CAPLUS <<LOGINID::20061108>>

DN 137:213205

TI Device for carrying out hybridization on microarrays
containing an agitation unit and sample dispenser

PA Tecan Trading Ag, Switz.

SO Ger. Gebrauchsmusterschrift, 27 pp. CODEN: GGXXFR

DT Patent

LA German

FAN.CNT 1	PATENT NO.	KIND	DATE	APPLICATION
NO.	DATE			

PI	DE 20207612	U1	20020919	DE 2002-20207612
	20020515			

PRAI	DE 2002-20207612	20020515
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AB The invention concerns a hybridization chamber for carrying
out reactions on microarrays of ***DNA*** and proteins or
tissues; the chamber is placed on the top of the
microarray in a way that it can be ***circularly***
moved relative to the chip in order to agitate the liq. that is
brought in contact with the probes that are immobilized on the
chip. There is a ring sealing between the chip and the chamber;
further parts are a sample application unit, fluid inflow and
outflow tubes, thermostat, etc. Agitation can also be performed
using a membrane pump.

L7 ANSWER 4 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN

AN 2002:624724 CAPLUS <<LOGINID::20061108>>

DN 137:290499

TI Brownian motion of ***DNA*** confined within a two-
dimensional array

AU Nykypanchuk, Dmytro; Strey, Helmut H.; Hoagland, David A.

CS Department of Polymer Science and Engineering, University
of Massachusetts Amherst, Amherst, MA, 01003, USA

SO Science (Washington, DC, United States) (2002), 297(5583),
987-990 CODEN: SCIEAS; ISSN: 0036-8075

PB American Association for the Advancement of Science

DT Journal

LA English

AB Linear ***DNA*** mols. are visualized while undergoing
Brownian motion inside media patterned with mol.-sized spatial
constraints. The media, prepd. by colloidal templating, trap the
macromols. within a two-dimensional ***array*** of spherical
cavities interconnected by ***circular*** holes. Across a
broad ***DNA*** size range, diffusion does not proceed by
the familiar mechanisms of reptation or sieving. Rather, because
of their inherent flexibility, ***DNA*** mols. strongly localize
in cavities and only sporadically "jump" through holes. Jumping
closely follows Poisson statistics. By reducing ***DNA*** 's
configurational freedom, the holes act as mol. wt.-dependent
entropic barriers. Sterically constrained macromol. diffusion
underlies many sepn. methods and assumes an important role in
intracellular and extracellular transport.

RE.CNT 30 THERE ARE 30 CITED REFERENCES AVAILABLE
FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE
FORMAT

L7 ANSWER 5 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN

AN 2001:644489 CAPLUS <<LOGINID::20061108>>

DN 135:206432

TI ***DNA*** array, ***DNA*** array reader, and
DNA array-manufacturing apparatus

IN Iwasaki, Yutaka; Suzuki, Yoshihiko

PA Nikon Corp., Japan

SO Jpn. Kokai Tokkyo Koho, 11 pp. CODEN: JKXXAF

DT Patent

LA Japanese

FAN.CNT 1	PATENT NO.	KIND	DATE	APPLICATION
NO.	DATE			

PI	JP 2001238674	A2	20010904	JP 2000-53312
	20000229			

PRAI	JP 2000-53312	20000229
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AB The conventional ***DNA*** array reader is
accompanied with the problem of not being able to perform the
reading with a high speed while maintaining a high S/N ratio such
as the one gained with a confocal microscope system. A
DNA array is provided, on which multiple spots of
DNA probes immobilized on the baseplate are
arrayed in a concentric ***circular*** shape, or a
spiral shape. A ***DNA*** array reader is provided, which
scans the spots of ***DNA*** probes with a high speed upon
turning the array while maintaining a high S/N ratio. Diagrams
describing the app. assembly are given.

L7 ANSWER 6 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN

AN 2001:319933 CAPLUS <<LOGINID::20061108>>

DN 134:348979

TI Protein and ***cDNA*** sequences of a novel human
circular canal protein 69 and diagnostic and therapeutic uses
thereof

IN Mao, Yumin; Xie, Yi

PA Shanghai Bio Road Gene Development Ltd., Peop. Rep.
China

SO PCT Int. Appl., 32 pp. CODEN: PIXXD2

DT Patent

LA Chinese

FAN.CNT 1 PATENT NO. KIND DATE APPLICATION
NO. DATE ----- ----- -----

PI WO 2001030823 A1 20010503 WO 2000-CN375
20001027 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR,
BY, BZ, CA, CH, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI,
GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP,
KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN,
MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK,
SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW,
AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS,
MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK,
ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF,
CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG CN 1303865
A 20010718 CN 1999-119866 19991027
PRAI CN 1999-119866 A 19991027

AB The invention provides protein and ***cDNA***
sequences for a novel human circular canal protein 69, which is a
novel member of kelch protein family. The circular canal protein
69 shares sequence homol. with Drosophila kelch protein. The
invention also relates to constructs and methods to express the
cloned gene for the prepn. of its protein and antibodies using
E.coli cells or eukaryotic cells, and diagnostic and therapeutic
uses for circular canal protein 69 related diseases.
RE.CNT 1 THERE ARE 1 CITED REFERENCES AVAILABLE FOR
THIS RECORD ALL CITATIONS AVAILABLE IN THE RE
FORMAT

L7 ANSWER 7 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:266132 CAPLUS <<LOGINID::20061108>>
DN 135:15553
TI SWI/SNF chromatin remodeling requires changes in
DNA topology
AU Gavin, Igor; Horn, Peter J.; Peterson, Craig L.
CS Program in Molecular Medicine Department of Biochemistry
and Molecular Biology, University of Massachusetts Medical
School, Worcester, MA, 01605, USA
SO Molecular Cell (2001), 7(1), 97-104 CODEN: MOCEFL; ISSN:
1097-2765
PB Cell Press
DT Journal
LA English

AB YSWI/SNF complex belongs to a family of enzymes that use
the energy of ATP hydrolysis to remodel chromatin structure.
Here we examine the role of ***DNA*** topol. in the
mechanism of ySWI/SNF remodeling. We find that the ability of
ySWI/SNF to enhance accessibility of nucleosomal ***DNA***
is nearly eliminated when ***DNA*** topol. is constrained in
small ***circular*** nucleosomal ***arrays*** and that
this inhibition can be alleviated by topoisomerases. Furthermore,
we demonstrate that remodeling of these substrates does not
require dramatic histone octamer movements or displacement.
Our results suggest a model in which ySWI/SNF remodels
nucleosomes by using the energy of ATP hydrolysis to drive local
changes in ***DNA*** twist.
RE.CNT 30 THERE ARE 30 CITED REFERENCES AVAILABLE
FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE
FORMAT

L7 ANSWER 8 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:266131 CAPLUS <<LOGINID::20061108>>
DN 135:15552
TI RSC unravels the nucleosome
AU Lorch, Yahli; Zhang, Mincheng; Kornberg, Roger D.
CS Department of Structural Biology, Stanford School of
Medicine, Stanford, CA, 94305, USA

SO Molecular Cell (2001), 7(1), 89-95 CODEN: MOCEFL; ISSN:
1097-2765

PB Cell Press
DT Journal
LA English
AB RSC and SWI/SNF chromatin-remodeling complexes were
previously reported to generate a stably altered nucleosome. We
now describe the formation of hybrids between nucleosomes of
different sizes, showing that the stably altered structure is a
noncovalent dimer. A basis for dimer formation is suggested by
an effect of RSC on the supercoiling of closed, ***circular***
arrays of nucleosomes. The effect may be explained by
the interaction of RSC with ***DNA*** at the ends of the
nucleosome, which could lead to the release 60-80 bp or more
from the ends. ***DNA*** released in this way may be
trapped in the stable dimer or lead to alternative fates such as
histone octamer transfer to another ***DNA*** or sliding
along the same ***DNA*** mol.
RE.CNT 34 THERE ARE 34 CITED REFERENCES AVAILABLE
FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE
FORMAT

L7 ANSWER 9 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:88435 CAPLUS <<LOGINID::20061108>>
DN 135:177087
TI Stability of a human SWI-SNF remodeled nucleosomal array
AU Guyon, Jeffrey R.; Narlikar, Geeta J.; Sullivan, E. Kelly;
Kingston, Robert E.
CS Department of Molecular Biology, Massachusetts General
Hospital, Boston, MA, 02114, USA
SO Molecular and Cellular Biology (2001), 21(4), 1132-1144
CODEN: MCEBD4; ISSN: 0270-7306
PB American Society for Microbiology
DT Journal
LA English
AB SWI-SNF alters ***DNA*** -histone interactions within a
nucleosome in an ATP-dependent manner. These alterations
cause changes in the topol. of a closed ***circular***
nucleosomal ***array*** that persist after removal of ATP
from the reaction. We demonstrate here that a remodeled closed
circular ***array*** will revert toward its original
topol. when ATP is removed, indicating that the remodeled array
has a higher energy than that of the starting state. However,
reversion occurs with a half-life measured in hours, implying a
high energy barrier between the remodeled and std. states. The
addn. of competitor ***DNA*** accelerates reversion of the
remodeled array by more than 10-fold, and we interpret this
result to mean that binding of human SWI-SNF (hSWI-SNF), even
in the absence of ATP hydrolysis, stabilizes the remodeled state.
In addn., we also show that SWI-SNF is able to remodel a closed
circular ***array*** in the absence of topoisomerase
I, demonstrating that hSWI-SNF can induce topol. changes even
when conditions are highly energetically unfavorable. We
conclude that the remodeled state is less stable than the std.
state but that the remodeled state is kinetically trapped by the
high activation energy barrier sepg. it from the unremodeled
conformation.
RE.CNT 51 THERE ARE 51 CITED REFERENCES AVAILABLE
FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE
FORMAT

L7 ANSWER 10 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2000:494777 CAPLUS <<LOGINID::20061108>>
DN 133:359597
TI Mammalian artificial chromosome formation from circular
aliphoid input ***DNA*** does not require telomere repeats

AU Ebersole, Thomas A.; Ross, Andrew; Clark, Elma; McGill, Niolette; Schindelhauer, Dirk; Cooke, Howard; Grimes, Brenda
CS MRC Human Genetics Unit, Western General Hospital, Edinburgh, EH4 2XU, UK
SO Human Molecular Genetics (2000), 9(11), 1623-1631
CODEN: HMGEE5; ISSN: 0964-6906
PB Oxford University Press
DT Journal
LA English
AB Mammalian artificial chromosomes (MACs) form in HT1080 cells after transfecting linear yeast artificial chromosome constructs minimally contg. competent alphoid arrays, a selectable marker and terminal human telomere repeats. Restrictions on the structure of input ***DNA*** in MAC formation were investigated by transfecting ***circular*** or linear alphoid constructs with or without human telomere ***arrays*** and by varying the position and orientation of the telomere arrays on input linear constructs. Circular input ***DNA*** efficiently produced MACs. Absence of telomere ***arrays*** from ***circular*** input mols. did not significantly alter MAC formation rates. Linear constructs capped with telomere arrays generated MACs effectively, but a severe redn. in MAC formation was obsd. from linear constructs lacking telomere arrays. Human telomere arrays positioned 1-5 kb from linear construct ends and in either orientation were able to promote MAC formation with similar efficiencies. Both circular and linear input constructs generated artificial chromosomes that efficiently segregated in the absence of selection. Telomeres were not detected on the MACs, regardless of the inclusion of telomere ***arrays*** on input ***DNA***, suggesting that ***circular*** chromosomes were formed. We found no evidence for acquisition of host cell ***DNA***, which is consistent with de novo chromosome assembly.
RE.CNT 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 11 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2000:305685 CAPLUS <<LOGINID::20061108>>
DN 133:256642
TI Gene delivery with optimized electroporation parameters shows potential for treatment of gliomas
AU Yoshizato, Kimio; Nishi, Toru; Goto, Tomoaki; Dev, Sukhendu B.; Takeshima, Hideo; Kino, Takeshi; Tada, Kenji; Kimura, Takahiro; Shiraishi, Shoji; Kochi, Masato; Kuratsu, Jun-ichi; Hofmann, Gunter A.; Ushio, Yukitaka
CS Department of Neurosurgery, Kumamoto University School of Medicine, Kumamoto, 860-8556, Japan
SO International Journal of Oncology (2000), 16(5), 899-905
CODEN: IJONES; ISSN: 1019-6439
PB International Journal of Oncology
DT Journal
LA English
AB Electroporation, a std. lab. method of introducing exogenous mols. into cells, has been gaining importance as a very effective non-viral phys. technique of gene delivery. In this study, we have used s.c. model of the C6 rat glioma cells and established an optimal condition to obtain very high gene expression in tumor tissues using both reporter and functional genes. Tumors grown on the flanks of Wistar rats are exposed and directly injected with plasmid ***DNA*** having the constructs of luciferase, green fluorescent protein and, the 'A' fragment of the diphtheria toxin, DT-A. The tumors are then subjected to square wave pulses from an electroporator. Gene expression is found to be several orders of magnitude higher when the tumors are pulsed with the optimized elec. parameters compared to the

controls. For luciferase, the enhancement is .apprx.135-fold, for the green fluorescent protein, gene expression is seen over a wide area within the sections examd., as contrast to a few punctate dots in the control specimens, and finally, DT-A shows massive death in the tumor tissue. A special ***circular*** ***array*** of six needles through which pulses are delivered with rotating elec. field is found to be highly efficient in transferring genes inside the tumor. Direct injection of plasmid ***DNA*** followed by electroporation allows very high in vivo gene transfer and its subsequent expression into tumor tissues. This method may be applicable to any solid tumor.
RE.CNT 56 THERE ARE 56 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 12 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1999:549456 CAPLUS <<LOGINID::20061108>>
DN 131:154464
TI A capillary electrophoresis apparatus for use in ***nucleic*** ***acid*** sequencing
IN Merenkova, Irena N.; Brevnov, Maxim
PA Tetragen, S.A., Russia
SO PCT Int. Appl., 47 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 3 PATENT NO. KIND DATE APPLICATION
NO. DATE -----

PI WO 9942819 A1 19990826 WO 1999-IB465
19990219 W: AU, CA, CN, JP, RU RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE US
6103083 A 20000815 US 1998-27426
19980220 CA 2320112 AA 19990826 CA 1999-
2320112 19990219 AU 9932692 A1 19990906 AU
1999-32692 19990219 AU 751105 B2 20020808
EP 1058841 A1 20001213 EP 1999-934340
19990219 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI JP 2002504681 T2 20020212
JP 2000-532710 19990219 RU 2217737 C2
20031127 RU 2000-123565 19990219
PRAI US 1998-27426 A 19980220 WO 1999-IB465
W 19990219
AB A capillary electrophoresis app. with a large no. of capillaries arranged in a curved, esp. ***circular***, ***array*** that may be used in ***DNA*** sequencing is described. The app. requires little supervision and can be used in high throughput sequencing projects. The present invention also relates to methods of using the electrophoresis app. and methods of making the electrophoresis app.
RE.CNT 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 13 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1999:529954 CAPLUS <<LOGINID::20061108>>
DN 131:295992
TI Structural analysis of adeno-associated virus transduction circular intermediates
AU Duan, Dongsheng; Yan, Ziyang; Yue, Yongping; Engelhardt, John F.
CS Department of Anatomy and Cell Biology and Department of Internal Medicine, The University of Iowa, Iowa City, IA, 52242, USA
SO Virology (1999), 261(1), 8-14 CODEN: VIRLAX; ISSN: 0042-6822
PB Academic Press

DT Journal
LA English

AB Recombinant adeno-assocd. virus (rAAV) has recently been demonstrated to form circular intermediates following transduction in muscle tissue and cell lines. Although restriction enzyme and Southern blot anal. has revealed a consistent monomer and multimer head-to-tail conformation, detailed structural sequence anal. has been lacking due to the high secondary structure of the ITR arrays. To gain further insight into potential mechanisms by which AAV circular genomes are formed from linear single-stranded viral *****DNA*****, we have performed chem. sequencing of ITR *****arrays***** within seven *****circular***** intermediates independently isolated from primary fibroblasts and Hela cells. Results from these studies demonstrated several types of circular intermediates with mosaic ITR elements flanked by two D sequences. The most predominant form consisted of a structure similar to that of previously generated AAV double-D plasmids, with one complete ITR flanked by two D-region elements. However, intermediately deleted ITR arrays with more than one complete ITR were also seen. Based on this structural information, we have proposed a model for formation of AAV circular intermediates by recombination/ligation between ITR ends of panhandle single-stranded AAV genomes. (c) 1999 Academic Press.

RE.CNT 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 14 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN AN 1997:751308 CAPLUS <<LOGINID::20061108>> DN 128:71592

TI The yeast silent information regulator Sir4p anchors and partitions plasmids

AU Ansari, Athar; Gartenberg, Marc R.

CS Department of Pharmacology, University of Medicine and Dentistry of New Jersey-Robert Wood Johnson Medical School, Piscataway, NJ, 08854, USA

SO Molecular and Cellular Biology. (1997), 17(12), 7061-7068 CODEN: MCEBD4; ISSN: 0270-7306

PB American Society for Microbiology

DT Journal

LA English

AB *****Circular***** plasmids contg. telomeric TG1-3 *****arrays***** or the HMR E silencer segregate efficiently between dividing cells of the yeast *Saccharomyces cerevisiae*. Subtelomeric X repeats augment the TG1-3 partitioning activity by a process that requires the SIR2, SIR3, and SIR4 genes, which are also required for silencer-based partitioning. Here we show that targeting Sir4p to *****DNA***** directly via fusion to the bacterial repressor LexA confers efficient mitotic segregation to otherwise unstable plasmids. The Sir4p partitioning activity resides within a 300-amino-acid region (residues 950 to 1262) which precedes the coiled-coil dimerization motif at the extreme carboxy end of the protein. Using a topol.-based assay, we demonstrate that the partitioning domain also retards the axial rotation of LexA operators in vivo. The anchoring and partitioning properties of LexA-Sir4p chimeras persist despite the loss of the endogenous SIR genes, indicating that these functions are intrinsic to Sir4p and not to a complex of Sir factors. In contrast, inactivation of the Sir4p-interacting protein Rap1p reduces partitioning by a LexA-Sir4p fusion. The data are consistent with a model in which the partitioning and anchoring domain of Sir4p (PAD4 domain) attaches to a nuclear component that divides sym. between cells at mitosis; *****DNA***** linked to Sir4p by LexA serves as a reporter of protein movement in these expts. We infer that the segregation behavior of telomere-

and silencer-based plasmids is, in part, a consequence of these Sir4p-mediated interactions. The assays presented herein illustrate two novel approaches to monitor the intracellular dynamics of nuclear proteins.

RE.CNT 71 THERE ARE 71 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 15 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN AN 1995:696723 CAPLUS <<LOGINID::20061108>> DN 123:164741

TI Protein phosphatase 2A, a potential regulator of actin dynamics and actin-based organelle motility in the green alga *Acetabularia*

AU Menzel, Diedrik; Vugrek, Oliver; Frank, Stefan; Elsner-Menzel, Christine

CS Max-Planck-Institut fur Zellbiologie, Ladenburg, D-68526, Germany

SO European Journal of Cell Biology (1995), 67(2), 179-87 CODEN: EJCBND; ISSN: 0171-9335

PB Wissenschaftliche Verlagsgesellschaft

DT Journal

LA English

AB The giant, unicellular alga *Acetabularia* is a well known exptl. model for the study of actin-dependent intracellular organelle motility. In the cyst stage, however, which is equiv. to the gametophytic stage, organelles are immobile, even though an actin cytoskeleton is present. The reason for the lack of organelle motility at this stage has not been known. To test the hypothesis that organelle motility could be under the control of posttranslational modification by protein phosphorylation, we have treated cysts with submicromolar concns. of okadaic acid or calyculin A, both potent inhibitors of serine/threonine protein phosphatases (ser/thr-PPases). The effects were dramatic: instead of linear actin bundles typical for control cysts, *****circular***** *****arrays***** of actin bundles formed in the cortical cyst cytoplasm. Concomitant with the formation of these actin rings, the cytoplasmic layers beneath the rings began to slowly rotate in a continuous and uniform counter-clockwise fashion. This effect suggests that protein phosphorylation acts on the actin cytoskeleton at two levels: (1) it changes the assembly properties of the actin filament system to the extent that novel cytoskeletal configurations are formed and (2) it raises the activity of putative motor proteins involved in the rotational movements to levels sufficiently high to support motility at a stage when organelle motility does not normally occur. Northern blot anal. of cyst stage-mRNA using probes specific to protein phosphatase type 1 (PP1) and type 2A (PP2A) reveals that PP2A is strongly expressed at this developmental stage whereas PP1 is not detectable, suggesting that PP2A is the likely target to the protein phosphatase inhibitors. As a first step in analyzing these regulatory proteins on the mol. level, we describe the complete sequence of a cyst-specific PP2A *****cDNA***** clone.

L7 ANSWER 16 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN AN 1995:578192 CAPLUS <<LOGINID::20061108>> DN 123:27138

TI Replication of an rRNA gene origin plasmid in the *Tetrahymena thermophila* macronucleus is prevented by transcription through the origin from an RNA polymerase I promoter

AU Pan, Wei-Jun; Gallagher, Renata C.; Blackburn, Elizabeth H. CS Dep. Microbiol. and Immunology, Univ. Calif., San Francisco, San Francisco, CA, 94143-0414, USA

SO Molecular and Cellular Biology (1995), 15(6), 3372-81 CODEN: MCEBD4; ISSN: 0270-7306

PB American Society for Microbiology
DT Journal
LA English

AB In the somatic macronucleus of the ciliate *Tetrahymena thermophila*, the palindromic rRNA gene (rDNA) minichromosome is replicated from an origin near the cent. of the mol. in the 5' nontranscribed spacer. The replication of this rDNA minichromosome is under both cell cycle and copy no. control. We addressed the effect on origin function of transcription through this origin region. A construct contg. a pair of 1.9-kb tandem direct repeats of the rDNA origin region, contg. the origin plus a mutated (+G), but not a wild type, rRNA promoter, is initially maintained in macronuclei as an episome. Later, linear and ***circular*** replicons with long ***arrays*** of tandem repeats accumulate (W.-J. Pan and E. H. Blackburn, ***Nucleic*** ***Acids*** Res, in press). We present direct evidence that the +G mutation inactivates this rRNA promoter. It lacks the footprint seen on the wild-type promoter and produces no detectable in vivo transcript. Independent evidence that the failure to maintain wild-type 1.9-kb repeats was caused by transcription through the origin came from placing a short ***DNA*** segment contg. the rRNA gene transcriptional termination region immediately downstream of the wild-type rRNA promoter. Insertion of this terminator sequence in the correct, but not the inverted, orientation restored plasmid maintenance. Hence, origin function was restored by inactivating the rRNA promoter through the +G mutation or causing termination before transcripts from a wild-type promoter reached the origin region. We propose that transcription by RNA polymerase I through the rDNA origin inhibits replication by preventing replication factors from assembling at the origin.

L7 ANSWER 17 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1995:349331 CAPLUS <<LOGINID::20061108>>
DN 122:128022

TI Computer simulation of the directional displacement of rod-shaped, arc-shaped, and ***circular*** objects in an ***array*** of obstacles, representing a simple model for the gel electrophoresis of small ***DNA***

AU Wheeler, David L.; Chrambach, Andreas
CS Sect. Macromol. Anal. Lab. Theor. Phys. Biol., Natl. Inst. Child Health Hum Dev. Natl. Inst. Health, Bethesda, MD, 20892-0001, USA
SO Biopolymers (1995), 35(2), 179-85 CODEN: BIPMAA; ISSN: 0006-3525
PB Wiley
DT Journal
LA English

AB The gel electrophoresis of ***DNA*** of identical length but various static conformations was simulated using a two-dimensional model of the movement of rod-shaped, arc-shaped, and ***circular*** objects through random ***arrays*** of disk-shaped obstacles. At low obstacle d., the displacement rate of these objects decreases from the rod-shaped to the circular approaches zero. The alignment of the arc-shaped objects along the axis of the directional movement of the objects was less than that achieved by the rod-shaped objects. Rod-shaped and arc-shaped objects were retarded in their movement by collisions with the obstacles; the no. of collisions of the former, in view of their greater ability to align, was less than that of the latter. Circular objects were exclusively retarded by collisions, while the arc-shaped objects exhibited an additional retarding mechanism, viz. the suspension ("hanging") on the obstacles. When the rigid objects were made flexible, their displacement increased. The increase was most pronounced with

the circular objects, allowing them to penetrate at obstacle densities from which the rigid objects were excluded.

L7 ANSWER 18 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1995:311260 CAPLUS <<LOGINID::20061108>>
DN 122:76335

TI Matching electrostatic charge between ***DNA*** and coat protein in filamentous bacteriophage. Fiber diffraction of charge-deletion mutants

AU Symmons, Martyn F.; Welsh, Liam C.; Nave, Colin; Marvin, Don A.; Perham, Richard N.

CS Cambridge Centre Molecular Recognition, Dep. Biochem., Univ. Cambridge, Cambridge, CB2 1QW, UK

SO Journal of Molecular Biology (1995), 245(2), 86-91 CODEN: JMOBAK; ISSN: 0022-2836

PB Academic

DT Journal

LA English

AB The virion of the Ff (fd, f1, M13) filamentous bacteriophage consists of a long tube of coat protein subunits in a shingled, helical ***array***, surrounding a genome of ***circular*** single-stranded ***DNA***. Modified fd virions have been generated by a mutation (K48A) that removes one pos. charge from each coat protein subunit in the C-terminal region of the polypeptide chain facing the ***DNA***. The no. of nucleotides in the mutant ***DNA*** is unchanged, but the K48A virions are 35% longer than the wild type. The authors measured the X-ray diffraction attributable to single virions in hydrated gels of wild-type and K48A bacteriophages. Most of the diffraction pattern shows no significant difference between wild-type and K48A. Since the ***DNA*** is only about 12% different by wt. of the wild-type virion, the diffraction pattern is dominated by the protein contribution, and the absence of significant differences indicates that there are no significant changes in the symmetry or structure of the protein coat. But there is a change in the diffraction pattern in a region where the ***DNA*** and protein contributions are comparable. The diffraction pattern of the K48A mutant shows an increase in intensity of one of the weaker equatorial peaks, relative to the wild type, in a region where the protein contribution has a neg. sign but the ***DNA*** contribution has a pos. sign. This is consistent with a decrease in the ratio of ***DNA***:protein per unit length of the K48A mutant. The results suggest that the protein forms a sheath lined with pos. charges interacting electrostatically and non-specifically with a neg. charged ***DNA*** core of matching charge d. The lower pos. charge d. lining the capsid in the K48A mutant means that correspondingly fewer nucleotides can be packaged per coat protein subunit, which in turn requires an elongation of the ***DNA*** inside the virion. A longer virion is thus required to package the same amt. of ***DNA***. Within the error of measurement, the no. of pos. charges on the protein interacting with the ***DNA*** is the same in K48A as in the wild type, despite the fact that the mutant is 35% longer than the wild type.

L7 ANSWER 19 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1990:459758 CAPLUS <<LOGINID::20061108>>
DN 113:59758

TI Adduct formation identification between phenyl glycidyl ether and 2'-deoxyadenosine and thymidine by chromatography, mass spectrometry and nuclear magnetic resonance spectroscopy

AU Van den Eeckhout, E.; De Bruyn, A.; Pepermans, H.; Esmans, E. L.; Vryens, I.; Claereboudt, J.; Claeys, M.; Sinsheimer, J. E.
CS Coll. Pharm., Univ. Ghent, Ghent, B-9000, Belg.

SO Journal of Chromatography (1990), 504(1), 113-28 CODEN: JOCRAM; ISSN: 0021-9673

DT Journal

LA English

AB Thymidine and 2'-deoxyadenosine were treated with Ph glycidyl ether in order to study the formation of the corresponding 2'-deoxynucleoside adducts. Sepn. methods were elaborated using either reversed-phase HPLC with photodiode-
array detection, or centrifugal *****circular***** TLC. The adducts were isolated on a preparative scale and were fully characterized by UV spectroscopy, desorption chem. ionization and fast atom bombardment mass spectrometry and 270- and 360-MHz 1H NMR spectrometry. For thymidine the main adduct was characterized as N-3-(2-hydroxy-3-phenoxypropyl)thymidine. With 2'-deoxyadenosine, predominantly N-1-(2-hydroxy-3-phenoxypropyl)-2'-deoxyadenosine was formed. With longer reaction times, the formation of a minor amt. of dialkylated 2'-deoxyadenosine was obsd. These nucleoside adducts will be used as marker compds. for studies of *****DNA***** adduct formation.

L7 ANSWER 20 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN AN 1986:511803 CAPLUS <<LOGINID::20061108>> DN 105:111803

TI *****DNA***** -protein interactions and *****DNA*****

packaging in filamentous bacteriophages

AU Rowitch, David H.; Hunter, Gary J.; Perham, Richard N.

CS Dep. Biochem., Univ. Cambridge, Cambridge, CB2 1QW, UK

SO Biochemical Society Transactions (1986), 14(6), 1168-9

CODEN: BCSTB5; ISSN: 0300-5127

DT Journal

LA English

AB The filamentous phages fd (infecting Escherichia coli) and Pf1 (infecting Pseudomonas aeruginosa) have genomes of *****circular*****, single-stranded *****DNA***** surrounded by a tubular *****array***** of .alpha.-helical coat protein subunits. The process of phage assembly is essentially the same in the 2 viruses. An obvious difference between the fd and Pf1 coat proteins is in the clustering of pos. charged side chains (lysine and arginine residues) in the C-terminal regions. The lysine at position 48 of the C-terminus of the fd coat protein was successfully mutated to arginine and glutamine, demonstrating that a pos. charge at this site is not essential for phage assembly. Genetic engineering expts. showed that the Pf1 coat protein could not be used efficiently in fd virion assembly.

L7 ANSWER 21 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN AN 1985:482492 CAPLUS <<LOGINID::20061108>> DN 103:82492

TI Restriction endonuclease map of pTiBo542, a potential Ti plasmid vector for genetic engineering of plants

AU Hood, Elizabeth E.; Jen, George; Kayes, Lucy; Kramer, Julie; Fraley, Robert T.; Chilton, Mary Dell

CS Dep. Biol., Washington Univ., St. Louis, MO, 63130, USA

SO Bio/Technology (1984), 2(8), 702-9 CODEN: BTCHDA; ISSN: 0733-222X

DT Journal

LA English

AB A phys. map was constructed for pTiBo542, a wide-host-range tumor-inducing plasmid of Agrobacterium tumefaciens. Forty-two fragments generated by the restriction endonuclease BamHI were arranged in a *****circular***** *****array***** using electrophoretic anal. of clones contg. overlapping segments of pTiBo542. The T- *****DNA***** region (the part of the Ti plasmid transferred to the plant) was predicted by its homol. to T- *****DNAs***** from heterologous octopine and nopaline Ti

plasmids. Southern hybridizations against soybean tumor *****DNA***** using clones from this region as probes confirmed this prediction.

L7 ANSWER 22 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN AN 1985:107185 CAPLUS <<LOGINID::20061108>>

DN 102:107185

TI Involvement of circular intermediates in the transfer of T-

*****DNA***** from Agrobacterium tumefaciens to plant cells

AU Koulikova-Nicola, Zdena; Shillito, Raymond D.; Hohn, Barbara; Wang, Kan; Van Montagu, Marc; Zembryski, Patricia

CS Friedrich-Miescher Inst., Basel, CH-4002, Peop. Rep. China

SO Nature (London, United Kingdom) (1985), 313(5999), 191-6

CODEN: NATUAS; ISSN: 0028-0836

DT Journal

LA English

AB The transfer of T- *****DNA***** from the Ti plasmid of Agrobacterium tumefaciens to Nicotiana tabacum plant cells was examd. for the presence of T- *****DNA***** intermediates. A *****DNA***** transformation assay was used to confirm the presence of circular intermediates. The structures may originate from circularization of T- *****DNA***** during induction of its transfer. These *****circular***** structures could produce tandem T- *****DNA***** *****arrays***** or multimeric *****circular***** structures suitable for the .lambda. packaging reaction. The circular intermediate junction site occurs precisely within the 25-base-pair terminal sequence essential for T- *****DNA***** transfer.

L7 ANSWER 23 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN AN 1983:103591 CAPLUS <<LOGINID::20061108>>

DN 98:103591

TI Radiation and biophysical studies on cells and viruses,

September 1, 1979-August 15, 1982

CS University of Texas, Houston, TX, USA

SO Report (1982), DOE/EV/02832-232; Order No. DE83000760,

10 pp. Avail.: NTIS From: Energy Res. Abstr. 1983, 8(1), Abstr.

No. 1045

DT Report

LA English

AB The objectives were to improve the understanding of the structure and organization of the chromatin of mammalian cells throughout the cell cycle, how radiation, chems., and heat damage these structures, and how cells repair the damage. Major accomplishments include evidence that chromatids contain 8 *****circular*****, duplex *****DNA***** mols. in a side-by-side *****array***** which are pleated to form loops by periodic attachments to a well-defined backbone structure. .gamma.-Ray-induced chromosomal damage was assayed as changes in the structure of dehistonized chromosomes. Bleomycin-induced damage to chromosomal loop structures was obsd., and heat treatment was shown to have affect on structural integrity.

L7 ANSWER 24 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN AN 1983:31310 CAPLUS <<LOGINID::20061108>>

DN 98:31310

TI Injection of *****DNA***** into liposomes by bacteriophage

.lambda.

AU Roessner, Charles A.; Struck, Douglas K.; Ihler, Garret M.

CS Dep. Med. Biochem., Texas A and M Coll. Med., College

Station, TX, 77843, USA

SO Journal of Biological Chemistry (1983), 258(1), 643-8

CODEN: JBCHA3; ISSN: 0021-9258

DT Journal

LA English

AB Small unilamellar vesicles (75-100 nm diam.) and large liposomes (>1 .mu.m in diam.) were prepd. contg. the lamB protein, an outer membrane protein of Escherichia coli and Shigella which serves as the receptor for bacteriophage .lambda.. Bacteriophage were obsd. to bind to these liposomes and vesicles by their tails and in most cases the heads of the bound bacteriophage appeared empty or partially empty of ***DNA***. The .lambda. ***DNA*** was usually only partially ejected from the bacteriophage head when small unilamellar liposomes were used, presumably because the vesicles are too small to contain all the ***DNA***. The partially ejected ***DNA*** was not susceptible to DNase unless the vesicle bilayer was 1st disrupted, suggesting that ***DNA*** injection of phage ***DNA*** into the vesicle had occurred. After disruption of these vesicles on electron microscope grids, the bacteriophage are seen to have partially empty heads and a small mass of ***DNA*** assocd. with their tails. Using larger liposomes prepd. by the fusion of lamB-bearing vesicles with polyethylene glycol and n-hexyl bromide, the heads of most of the bound bacteriophage appeared to be completely empty of ***DNA***. Disruption of these preps. on electron microscope grids revealed ***circular*** ***arrays*** of empty-headed bacteriophage surrounding ***DNA*** which had apparently been contained within the intact liposomes. Apparently high mol. wt. ***DNA*** can be entrapped within liposomes with high efficiency by ejection from bacteriophage .lambda.. The possible use of these ***DNA*** -contg. liposomes to facilitate gene transfer in eukaryotic cells is discussed.

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L1 779 S (CIRCULAR?(10A)(ARRAY? OR MICROARRAY?))/BI,AB

L2 1165 S PHAGEMID?/BI,AB

L3 1 S L1 AND L2

L4 701 S L1 NOT 2006/PY

L5 640 S L4 NOT 2005/PY

L6 569 S L5 NOT 2004/PY

L7 24 S L6 AND (DNA# OR CDNA# OR (NUCLEIC(W)ACID#))/BI,AB

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L2	37925	435/6[ccls]	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/11/08 09:19
L3	280	l1 and l2	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/11/08 09:20
L4	1214015	@rlad<"20030725"	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/11/08 09:20
L5	183	l3 and l4	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/11/08 09:35
L6	2	l5 and phagemid	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/11/08 09:36